IN THE SPECIFICATION

Please replace the paragraph at page 7, line 14, with the following rewritten paragraph:

Fig. 3 shows the second half of the post-amplification base sequence data according to the first embodiment (SEQ ID NO:1).

Please replace the paragraph at page 8, line 17, with the following rewritten paragraph:

Fig. 15 shows the second half of the pre-amplification base sequence data that serve as input data for the system for searching for relationships between base sequences according to the second embodiment (SEQ ID NO:2).

Please replace the paragraph at page 21, line 24 to page 22, line 14, with the following rewritten paragraph:

The 16S rDNA sequence data is downloaded genus by genus from the DNA information supplied by the National Institute of Agrobiological Sciences, Ministry of Agriculture and Fisheries, Japan. The DNA information supplied by the National Institute of Agrobiological Sciences is constructed based on the DNA information obtained from the Gene Bank (National Center for Biotechnology Information), DDBJ (National Institute of Genetics), and EMBL (European Molecular Biology Laboratory). Also, 5'-gctcagattgaacgctggcg-3' (SEQ ID NO:3) as the forward primer (41f), 5'-acatttcacaacacgagctg-3' (SEQ ID NO:4) as the reverse primer (1066r), and fourteen kinds of restriction enzymes were input. The region sandwiched by the forward primer and the reverse primer was extracted as post-amplification base sequence data 22b from the pre-amplification base sequence data 22a by the amplified sequence recognizing portion 31, and 357 genera, 1233 species, or 1503 kinds of base sequence data were obtained as the post-amplification base

sequence data 22b. Then, the lengths of fragments digested by the restriction enzymes were calculated and output as theoretical restriction fragment patterns by the theoretical value calculating portion 11.